

Input file Fbh21620fl.seq; Output File 21620.trans  
Sequence length 1909

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TACTTAGACTCAGCCGGCTTTTCCACGCTTTGCCTGACCCCTGCTTTGCTCAACTGTACGCTCTGTTTCGTTTTCTGTTC
TGCGCCGTTACAGATCCAAGCTCTGAAAAACCAGAAAGTTAACTGGTAAGTTTAGTCTTTTGTCTTTTATTTACAGGTC
CCGGATCCGGTGATCCAAATCTAAGAACTGCTCCTCAGTGAGTGTTCGCTTTACTTCTAGGCCTGTACGGAAGTGTAC
TTCTGCTCTAAAAGCTGCGGAATTCTAATACGACTCACTATAGGGAGTCGACCCACGGCTCCGGGGTCTAGGCGCGGAT
CGGACCCAAGCAGGTGCGGCGCGCGGCGGAGAGAGCGGCGGCGGTCAGCTCCTCGACCCCGTGTGCGGGCTAGTCCAG
      M A R P G M E R W R D R L
CGAGGCGGACGGGCGGCGTGGGCCC ATG GCC AGG CCC GGC ATG GAG CGG TGG CGC GAC CGG CTG 13
      39
A L V T G A S G G I G A A V A R A L V Q 33
CGC CTG GTG ACG GGG GCC TCG GGG GGC ATC GGC GCG GCC GTG GGC CGG GCC CTG GTC CAG 99
Q G L K V V G C A R T V G N I E E L A A 53
CAG GGA CTG AAG GTG GTG GGC TGC GCC CGC ACT GTG GGC AAC ATC GAG GAG CTG GCT GCT 159
E C K S A G Y P G T L I P Y R C D L S N 73
GAA TGT AAG AGT GCA GGC TAC CCC GGG ACT TTG ATC CCC TAC AGA TGT GAC CTA TCA AAT 219
E E D I L S M F S A I R S Q H S G V D I 93
GAA GAG GAC ATC CTC TCC ATG TTC TCA GCT ATC CGT TCT CAG CAC AGC GGT GTA GAC ATC 279
C I N N A G L A R P D T L L S G S T S G 113
TGC ATC AAC AAT GCT GGC TTG GCC CGG CCT GAC ACC CTG CTC TCA GGC AGC ACC AGT GGT 339
W K D M F N V N V L A L S I C T R E A Y 133
TGG AAG GAC ATG TTC AAT GTG AAC GTG CTG GCC CTC AGC ATC TGC ACA CGG GAA GCC TAC 399
Q S M K E R N V D D G H I I N I N S M S 153
CAG TCC ATG AAG GAG CGG AAT GTG GAC GAT GGG CAC ATC ATT AAC ATC AAT AGC ATG TCT 459
G H R V L P L S V T H F Y S A T K Y A V 173
GGC CAC CGA GTG TTA CCC CTG TCT GTG ACC CAC TTC TAT AGT GCC ACC AAG TAT GCC GTC 519
T A L T E G L R Q E L R E A Q T H I R A 193
ACT GCG CTG ACA GAG GGA CTG AGG CAA GAG CTT CGG GAG GCC CAG ACC CAC ATC CGA GCC 579
T C I S P G V V E T Q F A F K L H D K D 213
ACG TGC ATC TCT CCA GGT GTG GTG GAG ACA CAA TTC GCC TTC AAA CTC CAC GAC AAG GAC 639
P E K A A A T Y E Q M K C L K P E D V A 233
CCT GAG AAG GCA GCT GCC ACC TAT GAG CAA ATG AAG TGT CTC AAA CCC GAG GAT GTG GCC 699
E A V I Y V L S T P A H I Q I G D I Q M 253
GAG GCT GTT ATC TAC GTC CTC AGC ACT CCC GCA CAC ATC CAG ATT GGA GAC ATC CAG ATG 759
R P T E Q V T *
AGG CCC ACG GAG CAG GTG ACC TAG 261
83
TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCCTTCATGGCTTGCCCTCTGGATTTTAGGTGTTGATTTCTGG
ATCACGGGATACCACTTCTGTCCACACCCCGACCAGGGGCTAGAAAAATTTGTTTGAGATTTTATATCATCTTGTCAA
ATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTACTTGTTAACTTGTTTC

```

FIGURE 1

TTGTGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCC  
CCATCTTCTTGCACCTCAACGTCTGTGGCTYANGGGCTGGGGTGGCAGAGGGAGGCCTTCACCTTATATCTGTGTGTGT  
ATCCAGGGCTCCAGACTTCCCTCCTCTGCCCTGCCCCACTGCACCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAG  
CCCAGTCTTGGCTTCTTGTCCCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCT  
GGCCCAGTGGATTTCATGGTGATCATTAAAAAGAAAAATCGCAACCAAAAAAAAAAAAAAAAAAGGGCGGGCCGCTAGAC  
TAGTYTAGAGAAAAAACCTCCACACCTCCCCYBDAMMYTKACGCCGNACGCNANGGGGCAATCAAGGACGCT

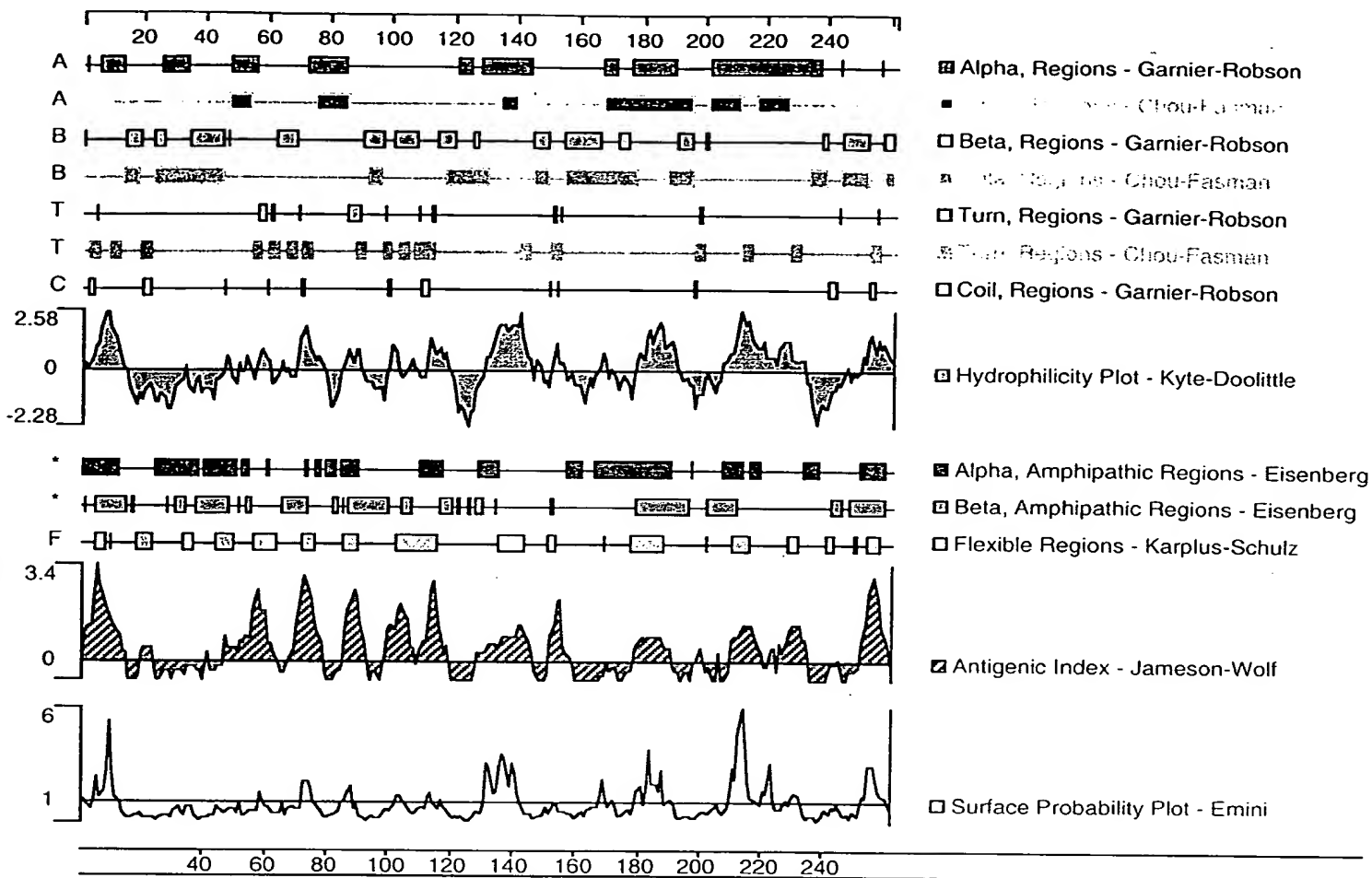
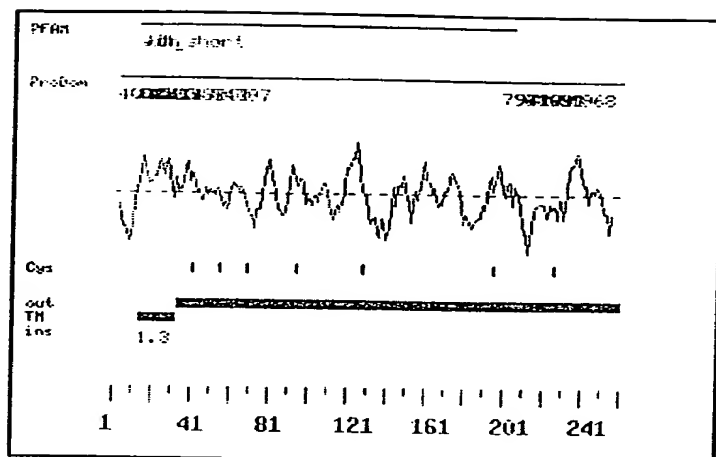


FIGURE 2

[Back to orfanat.cgi](#)

## Analysis of 21620 (260 aa)



### Signal Peptide Predictions for 21620

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

### Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
13	32	ins-->out	1.3

FIGURE 3

## Prosites Pattern Matches 21620

>P300055|PDOC00005|PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 135      SMK      137

>P300006|PDOC00006|CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 72      SNEE      75

Query: 89      SGVD      92

Analysis of 21620

Query: 135      SMKE      138

>P300008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 18      GASGGI      23

Query: 24      GAAVAR      29

Query: 40      GCARTV      45

Query: 90      GVDICI      95

Query: 109      GSTSGW      114

Query: 199      GVVETQ      204

>P300061|PDOC00060|ADH\_SHORT Short-chain alcohol dehydrogenase family signature.

Query: 166      YSATKYAVTAL      176

FIGURE 4

ADH21620

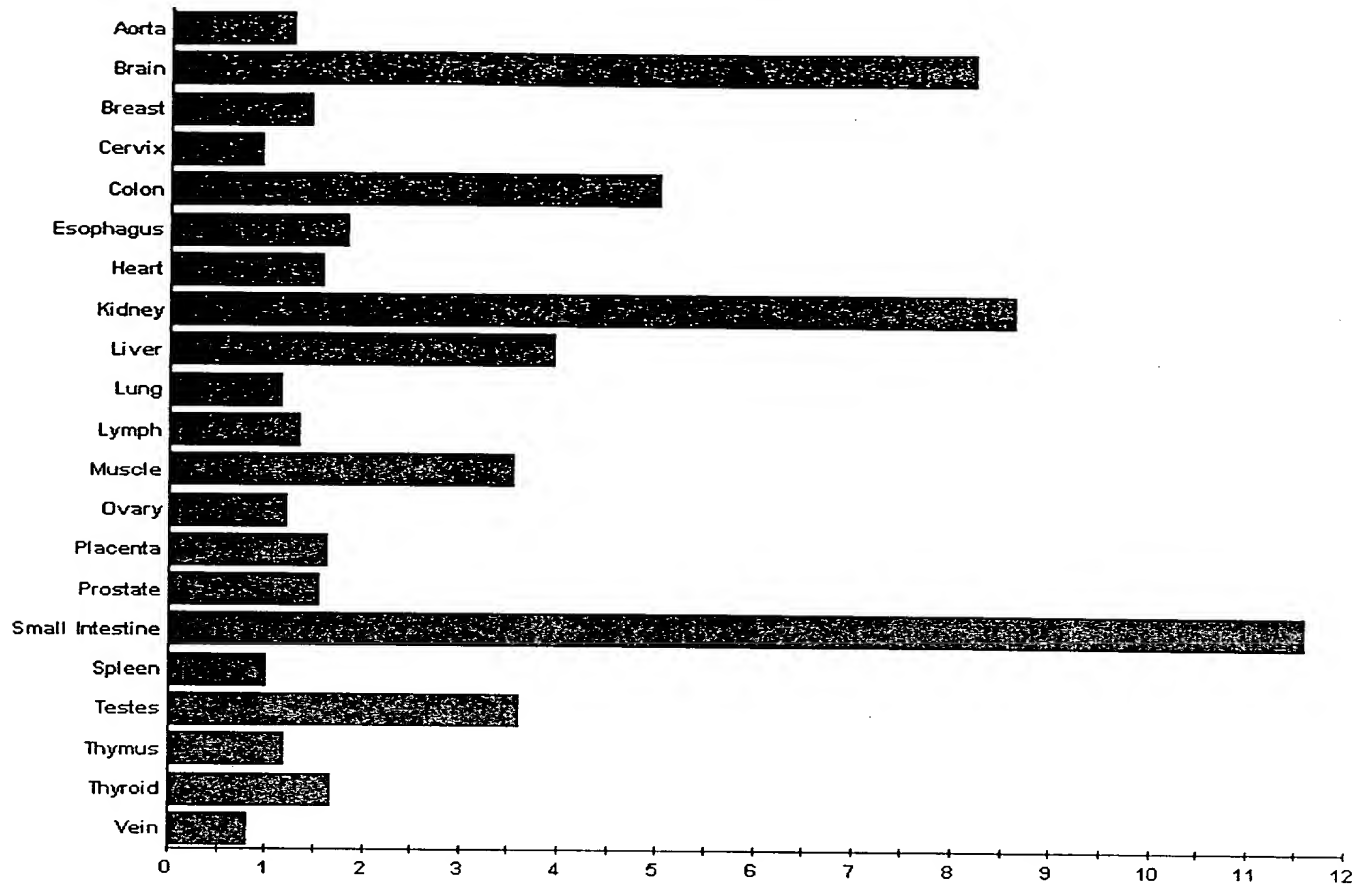


FIGURE 5

# 21620 Taqman Oncology Panel Expression

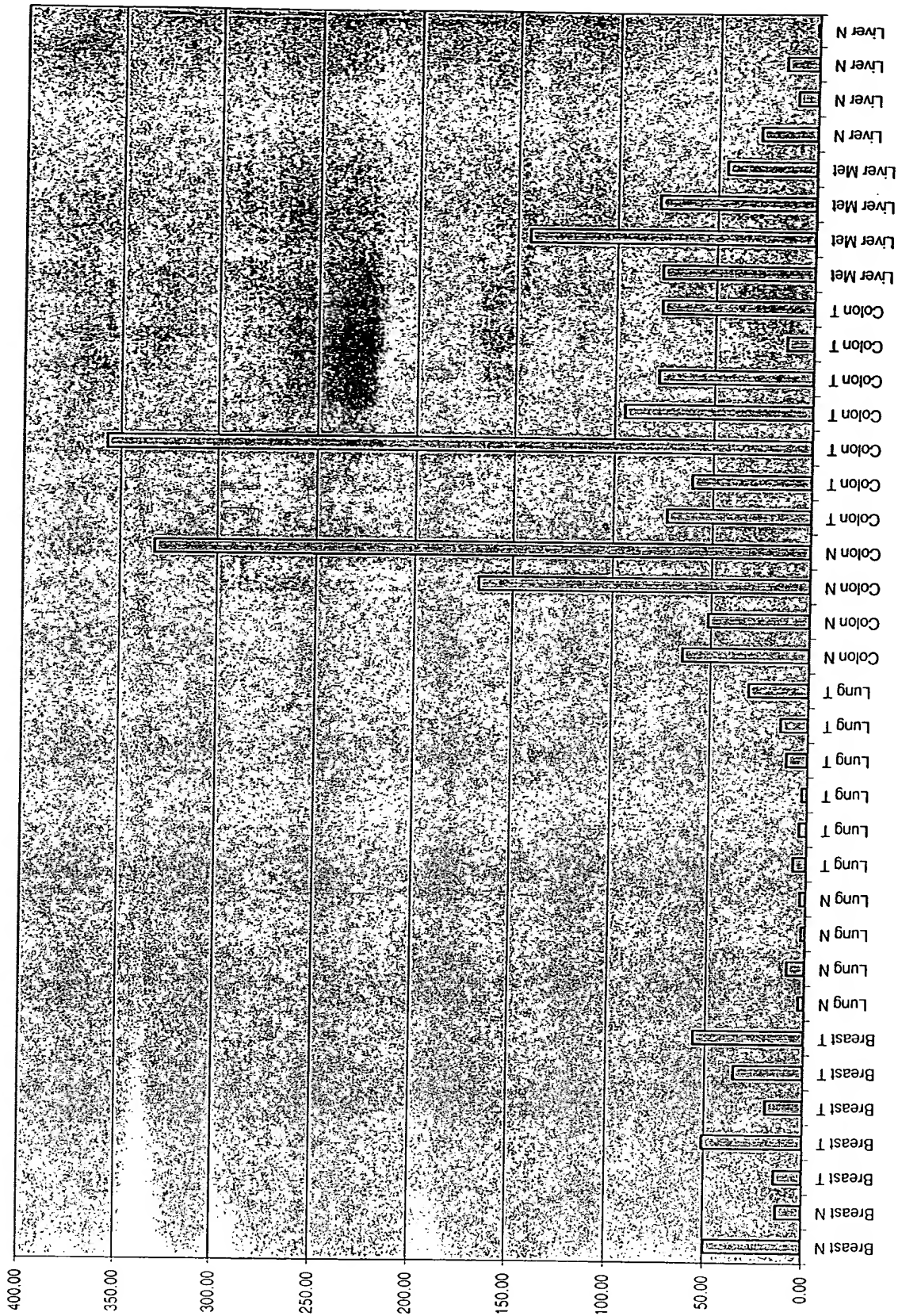


FIGURE 6

Input file Fbh33756.seq; Output File 33756.trans  
Sequence length 1153

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CCGCGCCCCCGCCTCGCAGCCCANNTNCGGACGCGGGCCCCAGCCGCGCCTGCGCTTCCGCTCGCCTGTGGCTGCAANNA
GCGCGCTCTTCTCGGAGCTACCCAGGCGGGCTGGTGTAGCAGCAAGCTCCGCGCCGACCCCTGACGCCCTGACGCCCTGTC
CCCGGCCCCGCGCATGAGCGCTACCTGCTGCCGCTGTCCGCGCTGGGCACGGTAGCAGGCGCTGCCCGTGTGCTCAAGA

      M E K C E A A A K D I R G 13
GGCAACATCATCCTGGCCTGCCGAGAC ATG GAG AAG TGT GAG GCG GCA GCA AAG GAC ATC CGC GGG 39

E T L N H H V N A R H L D L A S L K S I 33
GAG ACC CTC AAT CAC CAT GTC AAC GCC CGG CAC CTG GAC TTG GCT TCC CTC AAG TCT ATC 99

R E F A A K I I E E E E R V D I L I N N 53
CGA GAG TTT GCA GCA AAG ATC ATT GAA GAG GAG GAG CGA GTG GAC ATT CTA ATC AAC AAC 159

A G V M R C P H W T T E D G F E M Q F G 73
GCG GGT GTG ATG CGG TGC CCC CAC TGG ACC ACC GAG GAC GGC TTC GAG ATG CAG TTT GGC 219

V N H L G H F L L T N L L L D K L K A S 93
GTT AAC CAC CTG GGT CAC TTT CTC TTG ACA AAC TTG CTG CTG GAC AAG CTG AAA GCC TCA 279

A P S R I I N L S S L A H V A G H I D F 113
GCC CCT TCG CGG ATC ATC AAC CTC TCG TCC CTG GCC CAT GTT GCT GGG CAC ATA GAC TTT 339

D D L N W Q T R K Y N T K A A Y C Q S K 133
GAC GAC TTG AAC TGG CAG ACG AGG AAG TAT AAC ACC AAA GCC GCC TAC TGC CAG AGC AAG 399

L A I V L F T K E L S R R L Q G S G V T 153
GTC GCC ATC GTC CTC TTC ACC AAG GAG TTG AGC CGG CGG CTG CAA GGC TCT GGT GTG ACT 459

V N A L H P G V A R T E L G R H T G I H 173
GTC AAC GCC CTG CAC CCC GGC GTG GCC AGG ACA GAG CTG GGC AGA CAC ACG GGC ATC CAT 519

G S T F S S T T L G P I F W L L V K S P 193
GGC TCC ACC TTC TCC AGC ACC ACA CTC GGG CCC ATC TTC TGG CTG CTG GTC AAG AGC CCC 579

E L A A Q P S T Y L A V A E E L A D V S 213
GAG CTG GCC GCC CAG CCC AGC ACA TAC CTG GCC GTG GCG GAG GAA CTG GCG GAT GTT TCC 639

G K Y F D G L K Q K A P A P E A E D E E 233
GGA AAG TAC TTC GAT GGA CTC AAA CAG AAG GCC CCG GCC CCC GAG GCT GAG GAT GAG GAG 699

V A R R L W A E S A R L V G L E A P S V 253
GTG GCC CGG AGG CTT TGG GCT GAA AGT GCC CGC CTG GTG GGC TTA GAG GCT CCC TCT GTG 759

R E Q P L P R * 261
AGG GAG CAG CCC CTC CCC AGA TAA 783

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CCTCTGGAGCAGATTGTGAAAGCCAGGATGGCGCCTCCAGACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCA  
CTACCTGAGCCGGGAGACCCAGGACTG

FIGURE 7



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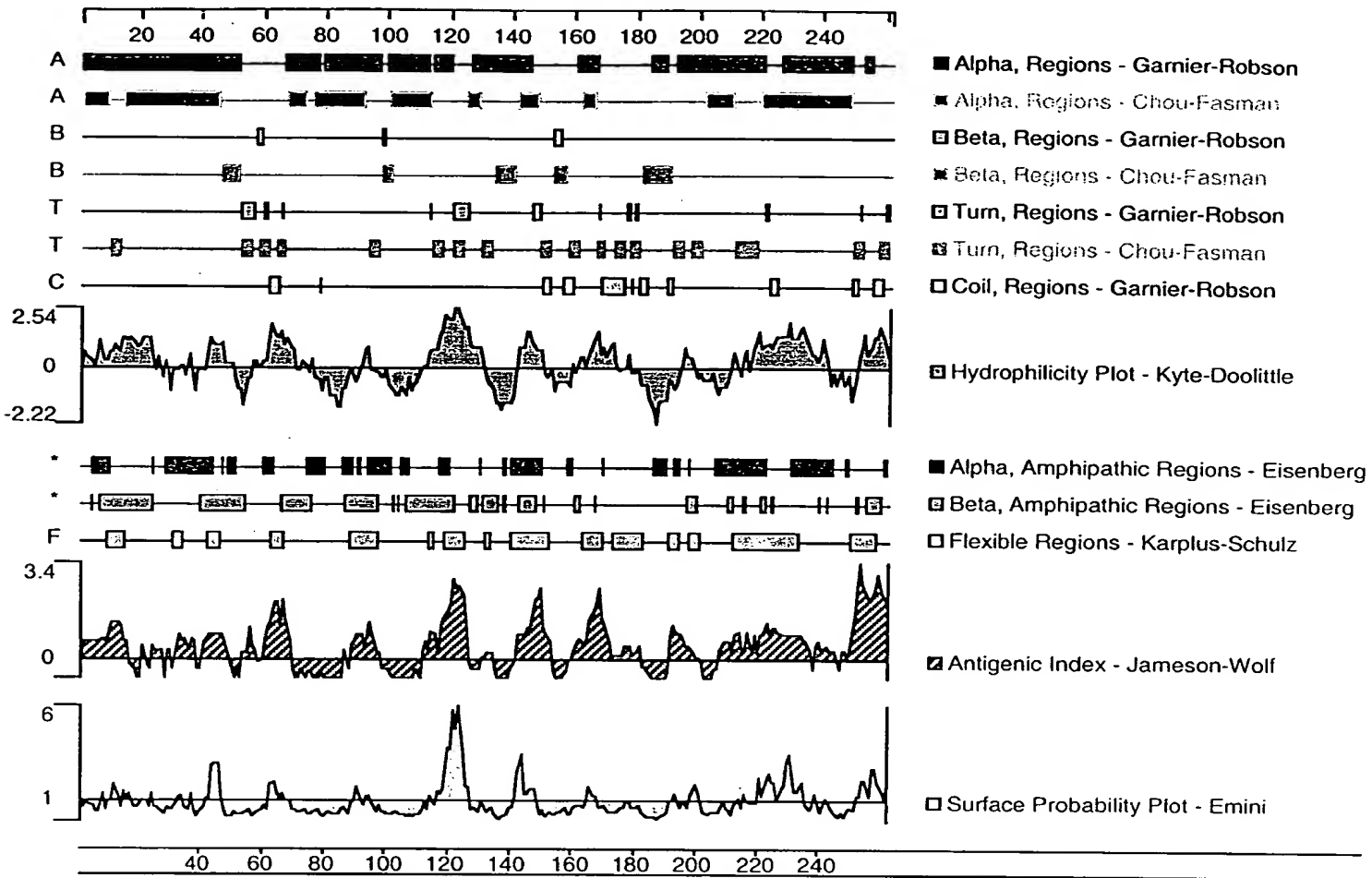
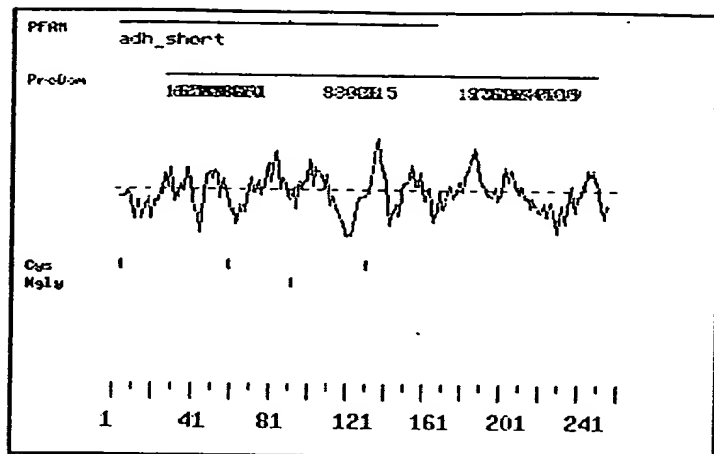


FIGURE 8

[Back to orfanat.cgi](#)

## Analysis of 33756 (260 aa)



---

### Signal Peptide Predictions for 33756

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

---

### No TM domains predicted by MEMSAT for 33756

---

**FIGURE 9**

# Prosite Pattern Matches for 3

>PDOC00001|PDOC00001|ASN\_GLYCOSYLATION N-glycosylation site.

Query: 100 NLSS 103

>PDOC00005|PDOC00005|PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 29 SLK 31

Query: 32 SIR 34

Query: 120 TRK 122

Query: 144 SRR 146

Query: 213 SGK 215

Query: 242 SAR 244

Query: 252 SVR 254

>PDOC00006|PDOC00006|CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 32 SIRE 35

Query: 63 TTED 66

Query: 252 SVRE 255

>PDOC00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 149 GSGVTV 154

Query: 160 GVARTE 165

Query: 171 GIHGST 176

FIGURE 10

Input file Fbh21676.seq; Output File 21676.trans  
Sequence length 1699

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GCNTGTGGGTCCCTTCTTNAATTGGGTCCCCCGTTTATAGGTAAGTTTAAAAGCTCAAGGTTCAAAGACNGGNCCTTT
TGTCGGGGGCTCCTTGAAGCCTACTAGATCANCGGCTCTCAGCTTTTTTTTTTGGGGNCCCCCCCCCTTTGGGAACCCC
CNTGGCTTTGCTTCAAACCTCTAAGGTCTTTTGTTCGTTCCTGCTGCGCGTTACAGATCCAAGYTCGAAAAA
CCAGAAAGTTAACTGGTAAGTTAGTCTTTTGTCTTTTATTTTCAGGTCCCGGATCCGGTGGTGGTGCAAATCAAAGAA
CTGCTCCTCAGTGGATGTTGCCCTTTACTTCTAGGCCCTGTACGAAGTGTACTTCTGCTCTAAAAGCTGCGGAATCTTAA
TACGACTCACTATAGGGAGTCGACCCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCGGAGCTACCCAGGCGGCTG

                                M   S   R   Y   4
GTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCCTGACGCCCTGACGCCCTGTCGCCCGCCCGGC ATG AGC CGC TAC 12

L   L   P   L   S   A   L   G   T   V   A   G   A   A   V   L   L   K   D   Y   24
CTG CTG CCG CTG TCG GCG CTG GGC ACG GTA GCA GGC GCC GCC GTG CTG CTC AAG GAC TAT 72

V   T   G   G   A   C   P   S   K   A   T   I   P   G   K   T   V   I   V   T   44
GTC ACC GGT GGG GCT TGC CCC AGC AAG GCC ACC ATC CCT GGG AAG ACG GTC ATC GTG ACG 132

G   A   N   T   G   I   G   K   Q   T   A   L   E   L   A   R   R   G   G   N   64
GGC GCC AAC ACA GGC ATC GGG AAG CAG ACC GCC TTG GAA CTG GCC AGG AGA GGA GGC AAC 192

I   I   L   A   C   R   D   M   E   K   C   E   A   A   A   K   D   I   R   G   84
ATC ATC CTG GCC TGC CGA GAC ATG GAG AAG TGT GAG GCG GCA GCA AAG GAC ATC CGC GGG 252

E   T   L   N   H   H   V   N   A   R   H   L   D   L   A   S   L   K   S   I   104
GAG ACC CTC AAT CAC CAT GTC AAC GCC CGG CAC CTG GAC TTG GCT TCC CTC AAG TCT ATC 312

R   E   F   A   A   K   I   I   E   E   E   E   R   V   D   I   L   I   N   N   124
CGA GAG TTT GCA GCA AAG ATC ATT GAA GAG GAG GAG CGA GTG GAC ATT CTA ATC AAC AAC 372

A   G   V   M   R   C   P   H   W   T   T   E   D   G   F   E   M   Q   F   G   144
GCG GGT GTG ATG CGG TGC CCC CAC TGG ACC ACC GAG GAC GGC TTC GAG ATG CAG TTT GGC 432

V   N   H   L   G   H   F   L   L   T   N   L   L   L   D   K   L   K   A   S   164
GTT AAC CAC CTG GGT CAC TTT CTC TTG ACA AAC TTG CTG CTG GAC AAG CTG AAA GCC TCA 492

A   P   S   R   I   I   N   L   S   S   L   A   H   V   A   G   H   I   D   F   184
GCC CCT TCG CGG ATC ATC AAC CTC TCG TCC CTG GCC CAT GTT GCT GGG CAC ATA GAC TTT 552

D   D   L   N   W   Q   T   R   K   Y   N   T   K   A   A   Y   C   Q   S   K   204
GAC GAC TTG AAC TGG CAG ACG AGG AAG TAT AAC ACC AAA GCC GCC TAC TGC CAG AGC AAG 612

L   A   I   V   L   F   T   K   E   L   S   R   R   L   Q   G   S   G   V   T   224
CTC GCC ATC GTC CTC TTC ACC AAG GAG CTG AGC CGG CGG CTG CAA GGC TCT GGT GTG ACT 672

V   N   A   L   H   P   G   V   A   R   T   E   L   G   R   H   T   G   I   H   244
GTC AAC GCC CTG CAC CCC GGC GTG GCC AGG ACA GAG CTG GGC AGA CAC ACG GGC ATC CAT 732

G   S   T   F   S   S   T   T   L   G   P   I   F   W   L   L   V   K   S   P   264
GGC TCC ACC TTC TCC AGC ACC ACA CTC GGG CCC ATC TTC TGG CTG CTG GTC AAG AGC CCC 792

E   L   V   A   Q   P   S   T   Y   L   A   V   A   E   E   L   A   D   V   S   284
GAG CTG GTC GCC CAG CCC AGC ACA TAC CTG GCC GTG GCG GAG GAA CTG CCG GAT GTT TCC 852

G   K   Y   F   D   G   L   K   Q   K   A   P   A   P   E   A   E   D   E   E   304

```

FIGURE 11

GGA AAG TAC TTC GAT GGA CTC AAA CAG AAG GCC CCG GCC CCC GAG GCT GAG GAT GAG GAG 912  
 V A R R L W A E S A R L V G L E A P S V 324  
 GTG GCC CGG AGG CTT TGG GCT GAA AGT GCC CGC CTG GTG GGC TTA GAG GCT CCC TCT GTG 972  
 R E Q P L P R \* 332  
 AGG GAG CAG CCC CTC CCC AGA TAA 996

CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAGACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCA  
 CTACCTGAGCCGGGAGACCCAGGACTGGCGCGCCTAGACTAGTCTAGAGAAAAACCTCCCACACCTCCCCCTGAACC  
 TGAAACAT

**FIGURE 11, Page 2**

21676.prot

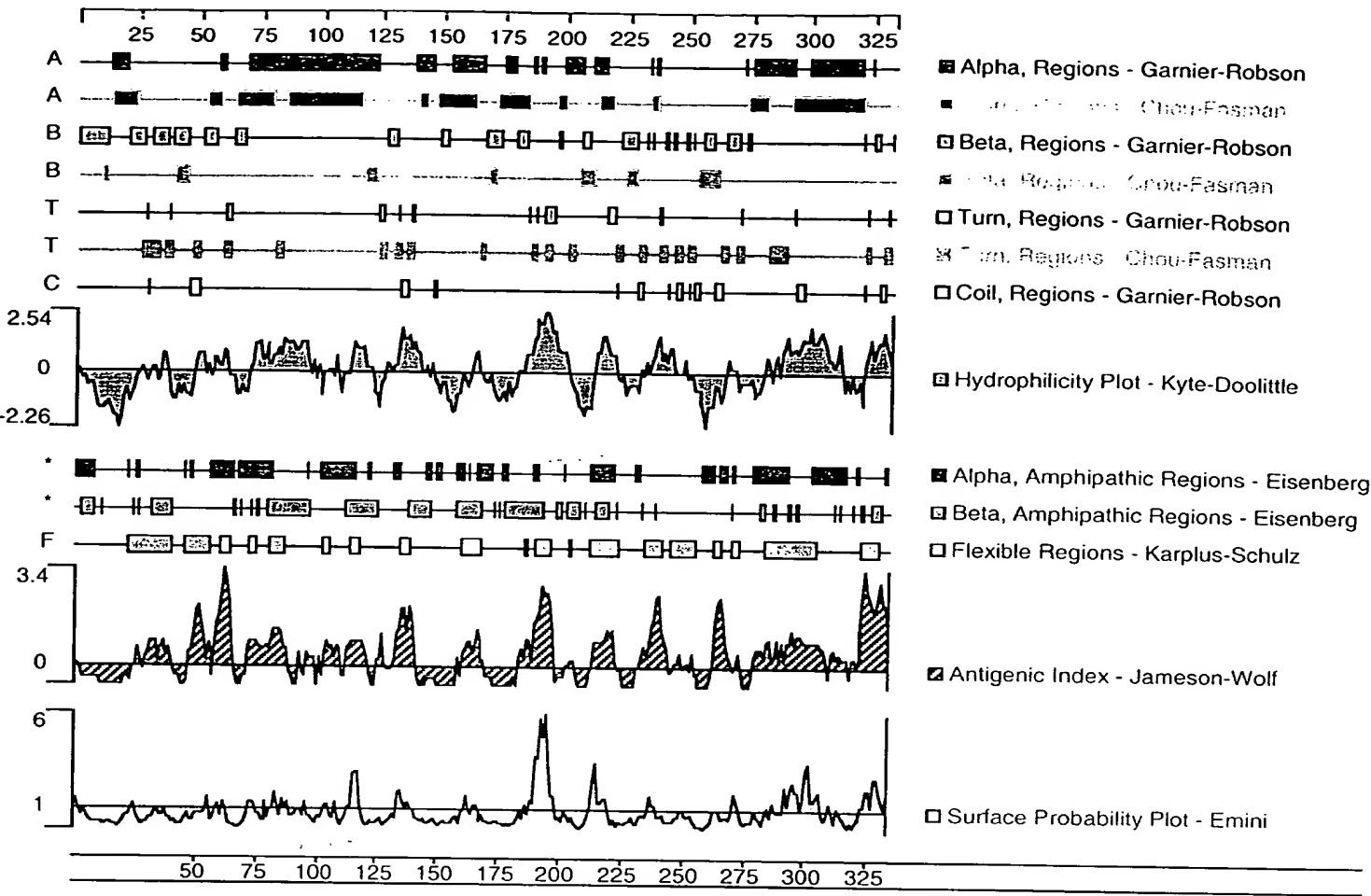
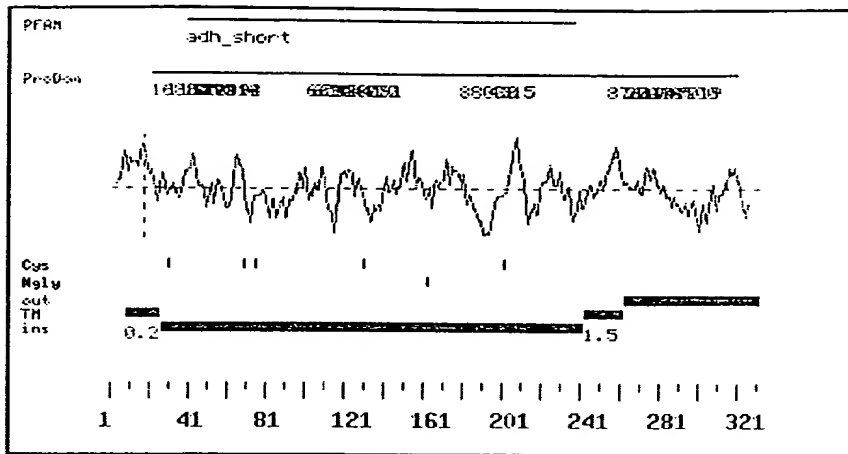


FIGURE 12

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## Analysis of 21676 (331 aa)



---

### Signal Peptide Predictions for 21676

Method	Predict	Score	Mat@
SignalP (eukaryote)	YES		17

Note: amino-terminal 70aa used for signal peptide prediction

---

### Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
8	25	out->ins	0.2
242	261	ins->out	1.5

### Transmembrane segments for presumed mature peptide

Start	End	Orient	Score
226	245	out->ins	2.1

## Prosites Pattern Matches for 21676

>PS00001|PDOC00001|ASN\_GLYCOSYLATION N-glycosylation site.

Query: 171 NLSS 174

>PS00005|PDOC00005|PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 100 SLK 102

Query: 103 SIR 105

Query: 191 TRK 193

Query: 215 SRR 217

Query: 284 SGK 286

Query: 313 SAR 315

Query: 323 SVR 325

>PS00006|PDOC00006|CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 54 TALE 57

Query: 103 SIRE 106

Query: 134 TTED 137

Query: 323 SVRE 326

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 12 GTVAGA 17

Query: 28 GACPSK 33

Query: 45 GANTGI 50

Query: 220 GSGVTV 225

Query: 231 GVARTE 236

Query: 242 GIHGST 247

FIGURE 14



Input file Fbh21612f11.seq; Output File 21612.trans  
Sequence length 2535

```

AGGCAGAAGTATGCAAAGCATGCATCTCAAATTAGTCAGCAAACCATAGTCCCGGCCCTAACTCCGCCCATCCCGCCC
CTAACTCCGNCCCAGTTCCGGCCCATTTCTCCGCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGCCGAGGCCGCC
TCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCTAGGCTTTTGCAAAAAGCTCCTCGATCGAG
GGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCGCCCATCCACGCCGGTTGAGTCGCGTTCTGCGGCC
TCCCGCCTGTGGTGCCCTCTGAAGTCGCTCCGCCGCTTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG
GCGCTCCCTTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCCTTG
TTTCAGTTTTCTGTCTCTGCGCCGTTACAGATCCAAGCTCTGAAAAACCAGAAAGTTAACTGGTAAGTTTAGTCCTTTTG
TCTTTTATTTTCAGGTCCCGGATCCGGTGGTGGTGCAAATCAAAGAACTGCTCCTCAGTGGATGTTGCCCTTACTTCTAG
GCCTGTACGGAAGTGTACTTCTGCTCTAAAAGCTGCGGAATTCTAATACGACTCACTATAGGGWGTGACCCACGCGT

                                M  L  P  N  T  G  R
CCGCTCGCCCGCCCGCTGTGCGCCGCCACCTCCTCTGATCTACGAAAGTC ATG TTA CCC AAC ACC GGG AGG      7
                                                                21

  L  A  G  C  T  V  F  I  T  G  A  S  R  G  I  G  K  A  I  A      27
CTG GCA GGA TGT ACA GTT TTT ATC ACA GGT GCA AGC CGT GGC ATT GGC AAA GCT ATT GCA      81

  L  K  A  A  K  D  G  A  N  I  V  I  A  A  K  T  A  Q  P  H      47
TTG AAA GCA GCA AAG GAT GGA GCA AAT ATT GTT ATT GCT GCA AAG ACC GCC CAG CCA CAT      141

  P  K  L  L  G  T  I  Y  T  A  A  E  E  I  E  A  V  G  G  K      67
CCA AAA CTT CTA GGC ACA ATC TAT ACT GCT GCT GAA GAA ATT GAA GCA GTT GGA GGA AAG      201

  A  L  P  C  I  V  D  V  R  D  E  Q  Q  I  S  A  A  V  E  K      87
GCC TTG CCA TGT ATT GTT GAT GTG AGA GAT GAA CAG CAG ATC AGT GCT GCA GTG GAG AAA      261

  A  I  K  K  F  G  G  I  D  I  L  V  N  N  A  S  A  I  S  L      107
GCC ATC AAG AAA TTT GGA GGA ATT GAT ATT CTG GTA AAT AAT GCC AGT GCC ATT AGT TTG      321

  T  N  T  L  D  T  P  T  K  R  L  D  L  M  M  N  V  N  T  R      127
ACC AAT ACA TTG GAC ACA CCT ACC AAG AGA TTG GAT CTG ATG ATG AAC GTG AAC ACC AGA      381

  G  T  Y  L  A  S  K  A  C  I  P  Y  L  K  K  S  K  V  A  H      147
GGC ACC TAC CTT GCA TCT AAA GCA TGT ATT CCT TAT TTG AAA AAG AGC AAA GTT GCT CAT      441

  I  L  N  I  S  P  P  L  N  L  N  P  V  W  F  K  Q  H  C  A      167
ATC CTC AAT ATC AGT CCA CCA CTG AAC CTA AAT CCA GTT TGG TTC AAA CAG CAC TGT GCT      501

  Y  T  I  A  K  Y  G  M  S  M  Y  V  L  G  M  A  E  E  F  K      187
TAT ACC ATT GCT AAG TAT GGT ATG TCT ATG TAT GTG CTT GGA ATG GCA GAA GAA TTT AAA      561

  G  E  I  A  V  N  A  L  W  P  K  T  A  I  H  T  A  A  M  D      207
GGT GAA ATT GCA GTC AAT GCA TTA TGG CCT AAA ACA GCC ATA CAC ACT GCT GCT ATG GAT      621

  M  L  G  G  P  G  I  E  S  Q  C  R  K  V  D  I  I  A  D  A      227
ATG CTG GGA GGA CCT GGT ATC GAA AGC CAG TGT AGA AAA GTT GAT ATC ATT GCA GAT GCA      681

  A  Y  S  I  F  Q  K  P  K  S  F  T  G  N  F  V  I  D  E  N      247
GCA TAT TCC ATT TTC CAA AAG CCA AAA AGT TTT ACT GGC AAC TTT GTC ATT GAT GAA AAT      741

  I  L  K  E  E  G  I  E  N  F  D  V  Y  A  I  K  P  G  H  P      267

```

FIGURE 15

ATC TTA AAA GAA GAA GGA ATA GAA AAT TTT GAC GTT TAT GCA ATT AAA CCA GGT CAT CCT	801
L Q P D F F L D E Y P E A V S K K V E S	287
TTG CAA CCA GAT TTC TTC TTA GAT GAA TAC CCA GAA GCA GTT AGC AAG AAA GTG GAA TCA	861
T G A V P E F K E E K L Q L Q P K P R S	307
ACT GGT GCT GTT CCA GAA TTC AAA GAA GAG AAA CTG CAG CTG CAA CCA AAA CCA CGT TCT	921
G A V E E T F R I V K D S L S D D V V K	327
GGA GCT GTG GAA GAA ACA TTT AGA ATT GTT AAG GAC TCT CTC AGT GAT GAT GTT GTT AAA	981
A T Q A I Y L F E L S G E D G G T W F L	347
GCC ACT CAA GCA ATC TAT CTG TTT GAA CTC TCC GGT GAA GAT GGT GGC ACG TGG TTT CTT	1041
D L K S K G G N V G Y G E P S D Q A D V	367
GAT CTG AAA AGC AAG GGT GGG AAT GTC GGA TAT GGA GAG CCT TCT GAT CAG GCA GAT GTG	1101
V M S M T T D D F V K M F S G K L K P T	387
GTG ATG AGT ATG ACT ACT GAT GAC TTT GTA AAA ATG TTT TCA GGG AAA CTA AAA CCA ACA	1161
M A F M S G K L K I K G N M A L A I K L	407
ATG GCA TTC ATG TCA GGG AAA TTG AAG ATT AAA GGT AAC ATG GCC CTA GCA ATC AAA TTG	1221
E K L M N Q M N A R L *	419
GAG AAG CTA ATG AAT CAG ATG AAT GCC AGA CTG TGA	1257

AGGAAAATATAAAAAAAGTCGACTGCTATGCTCAAAAAGTAAAAAAGCTCAACAGTTAAATCTAATGTTTGT  
 CTTTCCTGTTATATTATAAGGATATGCACGTTTGTCTCGAAAAGATAGAATTTGTCTCTAAAAGACTTGAAATGTAA  
 TTAAATGGCAAGCTAATCAAACATAAGCTTCATTAAGTGGGATCTAAGACAGTCGTGTTTTTATATTCAAGGGTT  
 TAACCCTTTGAGCCTTACATCTCATTCACTGTCTTTCTCCAAGAAAAGTATTTTGGGCGGACAGTCAGATCAAGCAGTA  
 AAATTAGCTCTTTCAAATCTTCTTGTCATGTAAAAATGAAGCTAGTCTGTTTAAAATTTTAGTTTGGATTGTATACT  
 AATGAAAATCTTAATGATGTTTTRWTTTATATACYTAWTTTWAARRAAWYYTWWWWWRKWCMTTTTWMCAAAA  
 TWTTAAAAAWKRRWWWKRYTSKSGMGRASWMAWRWRAMMC

FIGURE 15, Page 2

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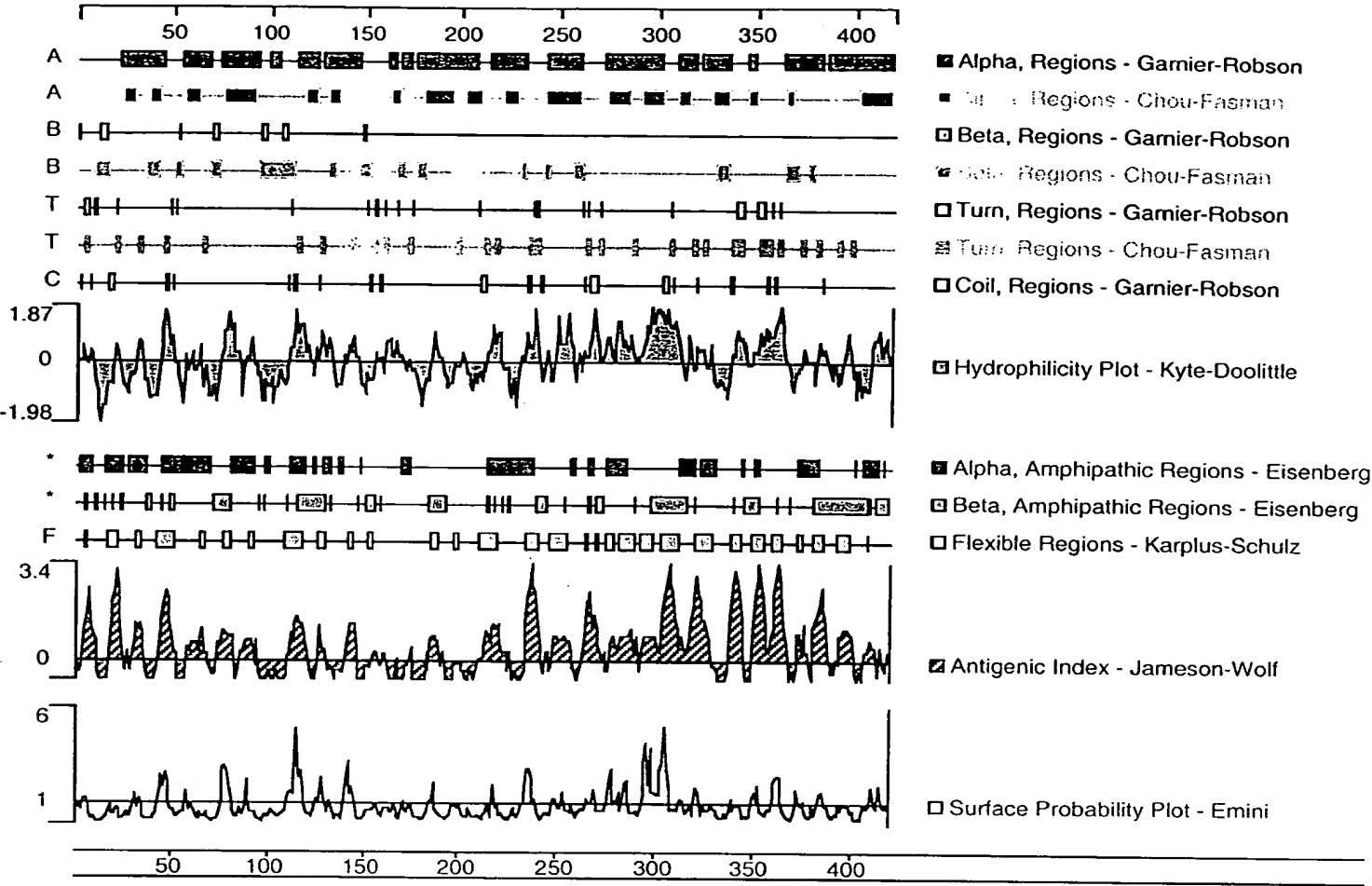
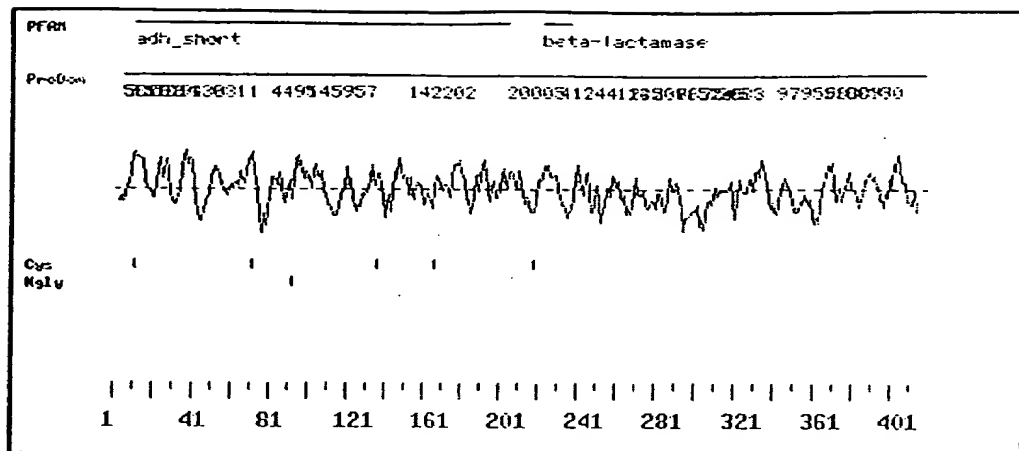


FIGURE 16

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## Analysis of 21612 (418 aa)



### Signal Peptide Predictions for 21612

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

No TM domains predicted by MEMSAT for 21612

FIGURE 17

## Prosites Pattern Match for 21612

>P500001|PDOC00001|ASN\_GLYCOSYLATION N-glycosylation site.

Query: 101 NASA 104

>P500005|PDOC00005|PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 5 TGR 7

Query: 115 TKR 117

Query: 282 SKK 284

Query: 313 TFR 315

Query: 381 SGK 383

Query: 392 SGK 394

>P500006|PDOC00006|CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 56 TAAE 59

Query: 320 SLSD 323

Query: 338 SGED 341

Query: 372 TTDD 375

>P500008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 17 GASRGI 22

Query: 52 GTIYTA 57

Query: 128 GTYLAS 133

Query: 353 GGNVGY 358

>P500242|PDOC00299|MICROBODIES\_CTER Microbodies C-terminal targeting signal.

Query: 416 ARL 418

FIGURE 18

> Fbh21615a - Import - complete

```

1      ATGCAAAAGC CGAGNCCGCC TCGGCCTCTA AGCTATTCCA GAAGTAGTAA GAAGGCTTTT
61     TTGAAGGCCT AGGCTTTTGC AAAAAGCTCC TCGATCGAGG GGCTCGCATC TCTCCTTCAC
121    GGGGCCGCGG CCCTACCTGA GGCCGCCATC CACGCCGGTT GAGTCGCGTT CTGCCGCCTC
181    CCGCCTGTGG TGCCTCCTGA ACTGCGTCCG CCGTYTAGGT AAGTTTAAAG CTCAGGTCGA
241    GACCGGGCCT TTGTCCGGCG CTCCCTTGGA GCCTACCTAG ACTCAGCCGG CTCTCCACGC
301    TTTGCCTGAC CCTGCTTGCT CAACTCTACG TCTTTGTTTC GTTTTCTGTT CTGCGCCGTT
361    ACAGATCCAA GCTCTGAAAA ACCAGAAAGT TAACTGGTAA GTTTAGTCTT TTTGTCTTTT
421    ATTTCAGGTC CCGGATCCGG TGGTGGTGCA AATCAAAGAA CTGCTCCTCA GTGGATGTTG
481    CCTTTACTTC TAGGCCTGTA CGGAAGTGTT ACTTCTGCTC TAAAAGCTGC GGAATTCCTAA
541    TACGACTCAC TATAGGGAGT CGACCCACGC GTCCGCAAAC CGAGTTCTGG AGAACGCCAT
601    CAGCTCGCTG CTTAAAATTA AACCACAGGT TCCATTATGG GTCGACTTGA TGGGAAAGTC
661    ATCATCCTGA CGGCCGCTGC TCAGGGGATT GGCCAAGCAG CTGCCTTAGC TTTTGCAAGA
721    GAAGGTGCCA AAGTCATAGC CACAGACATT AATGAGTCCA AACTTCAGGA ACTGGAAAAG
781    TACCCGGGTA TTCAAACTCG TGTCCTTGAT GTCACAAAGA AGAAACAAAT TGATCAGTTT
841    GCCAATGAAG TTGAGAGACT TGATGTTCTC TTTAATGTTG CTGGTTTTGT CCATCATGGA
901    ACTGTCCTGG ATTGTGAGGA GAAAGACTGG GACTTCTCGA TGAATCTCAA TGTGCGCAGC
961    ATGTACCTGA TGATCAAGGC ATTCCTTCCT AAAATGCTTG CTCAGAAATC TGGCAATATT
1021   ATCAACATGT CTTCTGTGGC TTCCAGCGTC AAAGGAGTTG TGAACAGATG TGTGTACAGC
1081   ACAACCAAGG CAGCCGTGAT TGGCCTCACA AAATCTGTGG CTGCAGATTT CATCCAGCAG
1141   GGCATCAGGT GCAACTGTGT GTGCCCAGGA ACAGTTGATA CGCCATCTCT ACAAGAAAGA
1201   ATACAAGCCA GAGGAAATCC TGAAGAGGCA CGGAATGATT TCCTGAAGAG ACAAAGACG
1261   GGAAGATTTC CAACTGCAGA AGAAATAGCC ATGCTCTGCG TGTATTGGC TTCTGATGAA
1321   TCTGCTTATG TAACTGGTAA CCCTGTCATC ATTGATGGAG GCTGGAGCTT GTGATTTTAG
1381   GATCTCCATG GTGGGAAGGA AGGCAGGCC TTCCTATCCA CAGTGAACCT GGTTACGAAG
1441   AAAACTCACC AATCATCTCC TTCCTGTTAA TCACATGTTA ATGAAAATAA GCTCTTTTTA
1501   ATGATGTCAC TGTTTGCAAG AGTCTGATTC TTTAAGTATA TTAATCTCTT TGTAATCTCT
1561   TCTGAAATCA TTGTAAAGAA ATAAAAATAT TGAACATAA AAAAAAAAAA AAAAAAGGGC
1621   GGCCGCTAGA CTAGTCTAGA GAAAAACCT CCCACACCTC CCCCTGAACC TGAAACATAA
1681   AATGAATGCM ATTGTTGKTG GTAAC TTGTT ATTGCA

```

FIGURE 19A

> Fbh21615a - Import - complete

MGR~~ED~~DGKV IILTAAAQGI QAAAALAFAR  
EGAKVIATDI NESKLQELEK YPGIQTRVLD VTKKKQIDQF ANEVERLDVL FNVAGFVHHG  
TVLDCEEKDW DFSMNLNVR MYLMIKAFLP KMLAQKSGNI INMSSVASSV KGVVNRVYS  
TTKAAVIGLT KSVAADFIQQ GIRCNCVCPG TVDTPSLQER IQARGNPEEA RNDFLKRQKT  
GRFATAEEIA MLCVYLASDE SAYVTGNPVI IDGGWSE\*

FIGURE 19B

21615prot

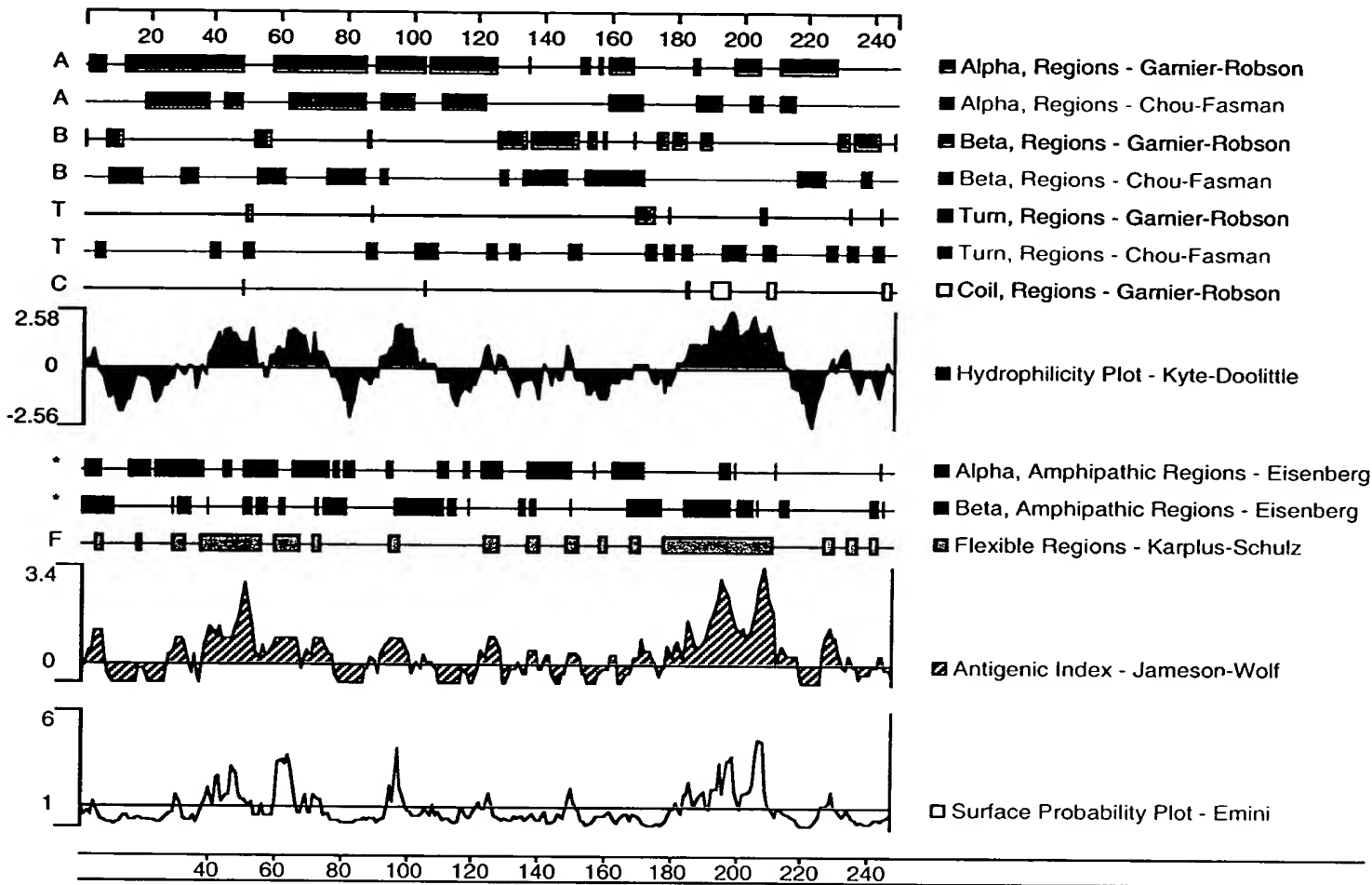
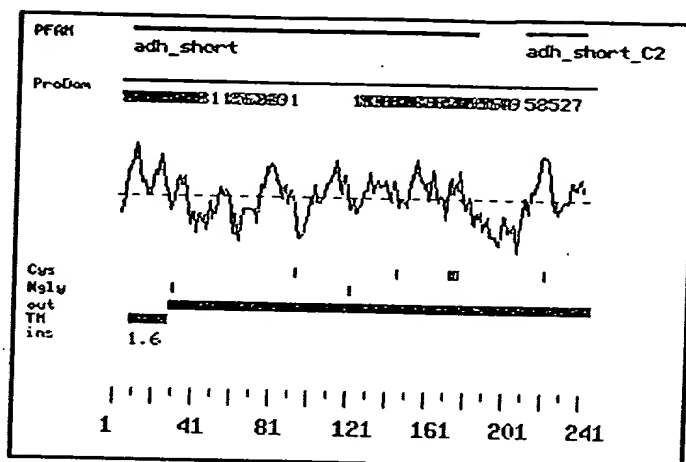


FIGURE 20



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## Analysis of 21615 (245 aa)



---

### Signal Peptide Predictions for 21615

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

---

### Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
8	27	ins-->out	1.6

FIGURE 21

## Prosites Pattern Matches for 21615

>PS00001|PDOC00001|ASN\_GLYCOSYLATION N-glycosylation site.

Query: 39 NESK 42

Query: 130 NMSS 133

>PS00005|PDOC00005|PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 60 TTK 62

Query: 137 SVK 139

Query: 149 TTK 151

Query: 208 TGR 210

>PS00006|PDOC00006|CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 89 TVLD 92

Query: 184 SLQE 187

Query: 213 TAEE 216

>PS00007|PDOC00007|TYR\_PHOSPHO\_SITE Tyrosine kinase phosphorylation site.

Query: 42 KLQELEKY 49

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 17 GIGQAA 22

Query: 126 GNIINM 131

Query: 156 GLTKSV 161

Query: 169 GIRCNC 174

>PS00061|PDOC00060|ADH\_SHORT Short-chain alcohol dehydrogenase family signature.

Query: 147 YSTTKAAVIGL 157

---

FIGURE 22

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